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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,123A

DATE: 02/27/2003

TIME: 10:56:32

Input Set : A:\Pg3606SEQLST.txt
Output Set: N:\CRF4\02272003\I857123A.raw

4 <110> APPLICANT: Glaxo Group Ltd
 5 Tate, Simon N
 6 Delany, Natalie S
 7 Sanseau, P
 9 <120> TITLE OF INVENTION: Novel Receptors
 11 <130> FILE REFERENCE: PG3606
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/857,123A
C--> 14 <141> CURRENT FILING DATE: 2000-06-01
 16 <150> PRIOR APPLICATION NUMBER: GB 9826359.3
 17 <151> PRIOR FILING DATE: 1998-12-01
 19 <160> NUMBER OF SEQ ID NOS: 40
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 4365
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (775)..(3294)
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 37 tgtataagct cagtggtctgt ggcagcgagg ttgaagagca aaggcaggcc gggcacctgg 180
 40 ctgatgtatgt gtggaccctgt tgccacagcg ggcggcactgt gcggtgtggg tgggggtggg 240
 42 ccagtcctctg ccgctcaccc tattccaggg acacagtctg cttggctctt ctggactgag 300
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 54 gttctagggg gctgggggca gcagcaagtt ggagtttgg ggtaccctgc ttcacaggc 660
 56 cttggcaag gagggcaggt ggggtctaag gacaagcagt cttactttg ggagtcaacc 720
 58 ccggcgtggc ggctgctgca ggttgcacac tggccacag agatccagc aagg atg 777
 59 Met
 60 1
 62 aag aaa tgg agc agc aca gac ttg ggg gca gct gcg gac cca ctc caa 825
 63 Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu Gln
 64 5 10 15
 66 aag gac acc tgc cca gac ccc ctg gat gga gac cct aac tcc agg cca 873
 67 Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg Pro
 68 20 25 30
 70 cct cca gcc aag ccc cag ctc tcc acg gcc aag agc cgc acc cgg ctc 921
 71 Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg Leu

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75	Phe	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Ala	Phe	Pro	Val	Asp	Cys	Pro	His		
76	50						55			60			65					
79	gag	gaa	ggg	ggt	gag	ctg	gac	tcc	tgc	ccg	acc	atc	aca	gtc	agc	cct	gtt	1017
80	Glu	Glu	Gly	Glu	Leu	Asp	Ser	Cys	Pro	Thr	Ile	Thr	Val	Ser	Pro	Val		
81							70			75			80					
83	atc	acc	atc	cag	agg	cca	gga	gac	ggc	ccc	acc	ggt	gcc	agg	ctg	ctg		1065
84	Ile	Thr	Ile	Gln	Arg	Pro	Gly	Asp	Gly	Pro	Thr	Gly	Ala	Arg	Leu	Leu		
85							85			90			95					
87	tcc	cag	gac	tct	gtc	gcc	gac	acc	gag	aag	acc	ctc	agg	ctc	tat		1113	
88	Ser	Gln	Asp	Ser	Val	Ala	Ala	Ser	Thr	Glu	Lys	Thr	Leu	Arg	Leu	Tyr		
89							100			105			110					
91	gat	cgc	agg	agt	atc	ttt	gaa	gcc	gtt	gct	cag	aat	aac	tgc	cag	gat		1161
92	Asp	Arg	Arg	Ser	Ile	Phe	Glu	Ala	Val	Ala	Gln	Asn	Asn	Cys	Gln	Asp		
93							115			120			125					
95	ctg	gag	agc	ctg	ctg	ctc	ttc	ctg	cag	aag	agc	aag	aag	cac	ctc	aca		1209
96	Leu	Glu	Ser	Leu	Leu	Leu	Phe	Leu	Gln	Lys	Ser	Lys	Lys	His	Leu	Thr		
97	130						135			140			145					
99	gac	aac	gag	ttc	aaa	gac	cct	gag	aca	ggg	aag	acc	tgt	ctg	ctg	aaa		1257
100	Asp	Asn	Glu	Phe	Lys	Asp	Pro	Glu	Thr	Gly	Lys	Thr	Cys	Leu	Lys			
101							150			155			160					
103	gcc	atg	ctc	aac	ctg	cac	gac	gga	cag	aac	acc	acc	atc	ccc	ctg	ctc		1305
104	Ala	Met	Leu	Asn	Leu	His	Asp	Gly	Gln	Asn	Thr	Thr	Ile	Pro	Leu	Leu		
105							165			170			175					
107	ctg	gag	atc	gcg	cgg	caa	acg	gac	ctg	aag	gag	ctt	gtc	aac	gcc		1353	
108	Leu	Glu	Ile	Ala	Arg	Gln	Thr	Asp	Ser	Leu	Lys	Glu	Leu	Val	Asn	Ala		
109							180			185			190					
111	agc	tac	acg	gac	tac	tac	aag	ggc	cag	aca	gca	ctg	cac	atc	gcc		1401	
112	Ser	Tyr	Thr	Asp	Ser	Tyr	Tyr	Lys	Gly	Gln	Thr	Ala	Leu	His	Ile	Ala		
113							195			200			205					
116	atc	gag	aga	cgc	aac	atg	gcc	ctg	gtg	acc	ctc	ctg	gtg	gag	aac	gga		1449
117	Ile	Glu	Arg	Arg	Asn	Met	Ala	Leu	Val	Thr	Leu	Leu	Val	Glu	Asn	Gly		
118	210						215			220			225					
120	gca	gac	gtc	cag	gct	gcg	gcc	cat	ggg	gac	ttc	ttt	aag	aaa	acc	aaa		1497
121	Ala	Asp	Val	Gln	Ala	Ala	Ala	His	Gly	Asp	Phe	Phe	Lys	Thr	Lys			
122							230			235			240					
124	ggg	cgg	cct	gga	ttc	tac	ttc	ggt	gaa	ctg	ccc	ctg	tcc	ctg	gcc	gcg		1545
125	Gly	Arg	Pro	Gly	Phe	Tyr	Phe	Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala		
126							245			250			255					
128	tgc	acc	aac	cag	ctg	ggc	atc	gtg	aag	ttc	ctg	ctg	cag	aac	tcc	tgg		1593
129	Cys	Thr	Asn	Gln	Leu	Gly	Ile	Val	Lys	Phe	Leu	Leu	Gln	Asn	Ser	Trp		
130							260			265			270					
132	cag	acg	gcc	gac	atc	agc	gcc	agg	gac	tcg	gtg	ggc	aac	acg	gtg	ctg		1641
133	Gln	Thr	Ala	Asp	Ile	Ser	Ala	Arg	Asp	Ser	Val	Gly	Asn	Thr	Val	Leu		
134							275			280			285					
136	cac	gcc	ctg	gtg	gag	gtg	gcc	gac	aac	acg	gcc	gac	aac	acg	aag	ttt		1689
137	His	Ala	Leu	Val	Glu	Val	Ala	Asp	Asn	Thr	Ala	Asp	Asn	Thr	Lys	Phe		
138	290						295			300			305					

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141	Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys	Leu His		
142	310	315	320	
144	ccg acg ctg aag ctg gag gag ctc acc aac aag aag gga	atg acg ccg	1785	
145	Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly	Met Thr Pro		
146	325	330	335	
148	ctg gct ctg gca gct ggg acc ggg aag atc ggg gtc ttg	gcc tat att	1833	
149	Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu	Ala Tyr Ile		
150	340	345	350	
153	ctc cag cgg gag atc cag gag ccc gag tgc agg cac	ctg tcc agg aag	1881	
154	Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His	Leu Ser Arg Lys		
155	355	360	365	
157	tcc acc gag tgg gcc tac ggg ccc gtg cac tcc	tcg ctg tac gac ctg	1929	
158	Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser	Leu Tyr Asp Leu		
159	370	375	380	385
161	tcc tgc atc gac acc tgc gag aag aac tcg	gtg ctg gag gtg atc gcc	1977	
162	Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu	Glu Val Ile Ala		
163	390	395	400	
165	tac agc agc agc gag acc cct aat cgc cac gac	atg ctc ttg gtg gag	2025	
166	Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp	Met Leu Leu Val Glu		
167	405	410	415	
169	ccg ctg aac cga ctc ctg cag gac aag tgg gac	aga ttc gtc aag cgc	2073	
170	Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg	Phe Val Lys Arg		
171	420	425	430	
173	atc ttc tac ttc aac ttc ctg gtc tac tgc	ctg tac atg atc atc ttc	2121	
174	Ile Phe Tyr Phe Asn Phe Leu Val Tyr Cys Leu	Tyr Met Ile Ile Phe		
175	435	440	445	
177	acc atg gct gcc tac tac agg ccc gtg gat ggc	ttg cct ccc ttt aag	2169	
178	Thr Met Ala Ala Tyr Tyr Arg Pro Val Asp Gly	Leu Pro Pro Phe Lys		
179	450	455	460	465
181	atg gaa aaa att gga gac tat ttc cga gtt act	gga gag atc ctg tct	2217	
182	Met Glu Lys Ile Gly Asp Tyr Phe Arg Val Thr	Gly Glu Ile Leu Ser		
183	470	475	480	
185	gtg tta gga gga gtc tac ttc ttc cga ggg	att cag tat ttc ctg	2265	
186	Val Leu Gly Gly Val Tyr Phe Phe Arg Gly	Ile Gln Tyr Phe Leu		
187	485	490	495	
190	cag agg cgg ccg tcg atg aag acc ctg ttt gtg	gac agc tac agt gag	2313	
191	Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val	Asp Ser Tyr Ser Glu		
192	500	505	510	
194	atg ctt ttc ttt ctg cag tca ctg ttc atg	ctg gcc acc gtg gtg ctg	2361	
195	Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu	Ala Thr Val Val Leu		
196	515	520	525	
198	tac ttc agc cac ctc aag gag tat gtg gct	tcc atg gta ttc tcc ctg	2409	
199	Tyr Phe Ser His Leu Lys Glu Tyr Val Ala Ser	Met Val Phe Ser Leu		
200	530	535	540	545
202	gcc ttg ggc tgg acc aac atg ctc tac tac acc	cgc ggt ttc cag cag	2457	
203	Ala Leu Gly Trp Thr Asn Met Leu Tyr Tyr Arg	Gly Phe Gln Gln		
204	550	555	560	
206	atg ggc atc tat gcc gtc atg ata gag aag	atg atc ctg aga gac ctg	2505	

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207	Met	Gly	Ile	Tyr	Ala	Val	Met	Ile	Glu	Lys	Met	Ile	Leu	Arg	Asp	Leu	
208	565						570						575				
210	tgc	cgt	ttc	atg	ttt	gtc	tac	atc	gtc	ttc	ttg	ttc	ggg	ttt	tcc	aca	2553
211	Cys	Arg	Phe	Met	Phe	Val	Tyr	Ile	Val	Phe	Leu	Phe	Gly	Phe	Ser	Thr	
212	580						585						590				
214	gct	gtg	gtg	acg	ctg	att	gaa	gac	ggg	aag	aat	gac	tcc	ctg	ccg	tct	2601
215	Ala	Val	Val	Thr	Leu	Ile	Glu	Asp	Gly	Lys	Asn	Asp	Ser	Leu	Pro	Ser	
216	595						600						605				
218	gag	tcc	acg	tcg	cac	agg	tgg	cg	ggg	cct	gcc	tgc	agg	ccc	ccc	gat	2649
219	Glu	Ser	Thr	Ser	His	Arg	Trp	Arg	Gly	Pro	Ala	Cys	Arg	Pro	Pro	Asp	
220	610						615						620			625	
222	agc	tcc	tac	aac	agc	ctg	tac	tcc	acc	tgc	ctg	gag	ctg	tcc	aag	ttc	2697
223	Ser	Ser	Tyr	Asn	Ser	Leu	Tyr	Ser	Thr	Cys	Leu	Glu	Leu	Phe	Lys	Phe	
224	630						635						640				
227	acc	atc	ggc	atg	ggc	gac	ctg	gag	ttc	act	gag	aac	tat	gac	ttc	aag	2745
228	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe	Thr	Glu	Asn	Tyr	Asp	Phe	Lys	
229	645						650						655				
231	gct	gtc	ttc	atc	atc	ctg	ctg	gcc	tat	gta	att	ctc	acc	tac	atc		2793
232	Ala	Val	Phe	Ile	Ile	Leu	Leu	Leu	Ala	Tyr	Val	Ile	Leu	Thr	Tyr	Ile	
233	660						665						670				
235	ctc	ctg	ctc	aac	atg	ctc	atc	gcc	ctc	atg	ggt	gag	act	gtc	aac	aag	2841
236	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu	Met	Gly	Glu	Thr	Val	Asn	Lys	
237	675						680						685				
239	atc	gca	cag	gag	agc	aag	aac	atc	tgg	aag	ctg	cag	aga	gcc	atc	acc	2889
240	Ile	Ala	Gln	Glu	Ser	Lys	Asn	Ile	Trp	Lys	Leu	Gln	Arg	Ala	Ile	Thr	
241	690						695						700			705	
243	atc	ctg	gac	acg	gag	aag	agc	ttc	ctt	aag	tgc	atg	agg	aag	gcc	ttc	2937
244	Ile	Leu	Asp	Thr	Glu	Lys	Ser	Phe	Leu	Lys	Cys	Met	Arg	Lys	Ala	Phe	
245	710						715						720				
247	cgc	tca	ggc	aag	ctg	ctg	cag	gtg	ggg	tac	aca	cct	gat	ggc	aag	gac	2985
248	Arg	Ser	Gly	Lys	Leu	Leu	Gln	Val	Gly	Tyr	Thr	Pro	Asp	Gly	Lys	Asp	
249	725						730						735				
251	gac	tac	cg	tgg	tgc	ttc	agg	gtg	gac	gag	gtg	aac	tgg	acc	acc	tgg	3033
252	Asp	Tyr	Arg	Trp	Cys	Phe	Arg	Val	Asp	Glu	Val	Asn	Trp	Thr	Thr	Trp	
253	740						745						750				
255	aac	acc	aac	gtg	ggc	atc	atc	aac	gaa	gac	ccg	ggc	aac	tgt	gag	ggc	3081
256	Asn	Thr	Asn	Val	Gly	Ile	Ile	Asn	Glu	Asp	Pro	Gly	Asn	Cys	Glu	Gly	
257	755						760						765				
259	gtc	aag	cgc	acc	ctg	agc	ttc	tcc	ctg	cg	tca	agc	aga	gtt	tca	ggc	3129
260	Val	Lys	Arg	Thr	Leu	Ser	Phe	Ser	Leu	Arg	Ser	Ser	Arg	Val	Ser	Gly	
261	770						775						780			785	
264	aga	cac	tgg	aag	aac	ttt	gcc	ctg	gtc	ccc	ctt	tta	aga	gag	gca	agt	3177
265	Arg	His	Trp	Lys	Asn	Phe	Ala	Leu	Val	Pro	Leu	Leu	Arg	Glu	Ala	Ser	
266	790						795						800				
268	gct	cga	gat	agg	cag	tct	gct	cag	ccc	gag	gaa	gtt	tat	ctg	cga	cag	3225
269	Ala	Arg	Asp	Arg	Gln	Ser	Ala	Gln	Pro	Glu	Glu	Val	Tyr	Leu	Arg	Gln	
270	805						810						815				
272	ttt	tca	ggg	tct	ctg	aag	cca	gag	gac	gct	gag	gtc	ttc	aag	agt	cct	3273
273	Phe	Ser	Gly	Ser	Leu	Lys	Pro	Glu	Asp	Ala	Glu	Val	Phe	Lys	Ser	Pro	

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274	820	825	830	
276	gcc gct tcc ggg gag aag tga ggacgtcacg	cagacagcac tgtcaacact		3324
277	Ala Ala Ser Gly Glu Lys			
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280	gggccttagg agacccgtt gccacgggg gctgctgagg	gaacaccagt gctctgtcag	3384	
282	cagcctggcc tggctgtgc ctgcccagca tgccccaaa	tctgtgtgg acaagctgtg	3444	
284	ggaagcgttc ttggaagcat ggggagtgtat	gtacatccaa ccgtcaactgt	3504	
286	atctcctaact agactttcag gtttttactc actttactaa	acagtttggaa tggtcagtct	3564	
288	ctactgggac atgttaggccc ttgttttctt ttgattttat	tcttttctgt gagacagagt	3624	
290	tcactcttgc tgcccaggct ggagtgcagt ggtgtatct	tggctcaactg caacctctgc	3684	
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307	caagctgttg cagcagtgcc ttcttcatcc ttcccttacga	tcaatcacag tctccagaag	4164	
309	atcagctcaa ttgctgtgca ggttaaaact acagaaccac	atcccaaagg tacctggtaa	4224	
311	gaatgttga aagatcttcc atttcttagga accccagttcc	tgcttctccg caatggcaca	4284	
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328	20 25 30			
330	Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg			
331	35 40 45			
333	Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro			
334	50 55 60			
336	His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro			
337	65 70 75 80			
339	Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu			
340	85 90 95			
342	Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu			
343	100 105 110			
345	Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln			
346	115 120 125			
348	Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu			
349	130 135 140			
351	Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu			
352	145 150 155 160			
354	Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu			
355	165 170 175			

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date